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Parental Selection for Breeding High Yielding and Drought Tolerant Lines through Genetic Diversity Studies in Mungbean (*Vigna radiata* L. Wilczek)

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ABSTRACT

Genetic divergence among thirty one genotypes was estimated using Mahalanobis's D^2 statistic. All the thirty one genotypes were grouped into seven clusters. Cluster II contained the highest number of ten genotypes followed by cluster III with eight genotypes. The patterns of distribution of genotypes from different geographical locations into seven clusters were random, demonstrating that geographical isolation may not be the only factor causing genetic diversity. The highest intra-cluster distance was observed for cluster IV (187.85) and the lowest was observed for cluster I (63.29). While the highest inter-cluster distance was observed between cluster IV and VII (663.76). Seed yield contributed maximum to diversity. Cluster III recorded the highest mean for seed yield per plant followed by days to maturity and number of seeds per pod. Hybridization programme may be initiated between PUSA VISHAL X TLM 7 (cluster IV X cluster VII) in order to get transgressive seggregants for drought tolerance since, these genotypes showed maximum diversity among themselves with desirable yield and drought parameters.

Key words : D^2 analysis, Genetic divergence, Mungbean.

Mungbean (*Vigna radiata* L. Wilczek; 2n= 22) is an important pulse crop which is widely cultivated and consumed throughout India. It is a protein rich staple food containing 23-25 per cent protein with high lysine content. Due to its short duration growth, nitrogen fixing capability, soil reinforcement and prevention of soil erosion, it is superior to other legumes. However, its production potential was reduced due to abiotic stress like drought. Many breeding programmes have been initiated to develop drought tolerant/ resistant varieties in mungbean. However, the progress is not significant as the drought is a complex phenomenon and always coupled with moisture and high temperature stresses. Therefore, systematic efforts are needed to breed the cultivars for high yield coupled with drought tolerance.

To initiate any breeding programme, genetic assessment and understanding of diverse mungbean cultivars for drought and high yield is essential to identify and concentrate on the important traits that could contribute to optimum yields under drought. Choosing genetically diverse parents will enable the expansion of genetic base and helps in development of superior genotypes. Keeping this in view, the present study was undertaken to estimate the genetic diversity on yield and drought contributing characters using Mahalanobi's D^2 statistic.

MATERIAL AND METHODS

The experimental material for the present investigation consisted of thirty one mungbean genotypes obtained from Regional Agricultural Research Station, Lam, Guntur and Agricultural Research Station, Madira. The experiment was conducted in randomized block design (RBD) with three replications during *kharif,* 2012-13 at wet land farm, Sri Venkateswara Agricultural College, Tirupati. Each genotype was sown in three rows of 4m length with a spacing of 30 cm between rows and 10 cms between plants within rows. Observations were recorded on five randomly selected plants per replication for traits namely, plant height, , number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, hundred seed weight, harvest index, SPAD Chlorophyll Meter Reading(SCMR), Relative Water Content (RWC), Relative Injury percentage(RI), Chlorophyll Stability Index (CSI) and Specific Leaf Area (SLA).Whereas, for days to 50% flowering and days to maturity observations were recorded on plot basis. The mean values for each character over the replications were subjected

Table 1. Cluster composition of thirty one mungbean genotypes.

Cluster No.	No. of genotypes	Genotypes
I	4	PUSA 9531, TM 96-2, COGG 974, LGG 410
II	10	MH-3-18, MH-565, IPM-02-03, LGG 407, LGG 460, MGG350, ML145,WGG-37, VG- 6197A,VG 7098A
III	8	ML-267, MGG347, MGG295, PM110, KM-122, WGG 2, RMG 492, IPM-02-19
IV	6	KM-8-657, LGG 450, GIVT 203, ASHA, PUSA VISHAL, LGG 528
V	1	EC- 396117
VI	1	AKM 9904
VII	1	TLM-7

Table 2. Intra cluster (diagonal) and inter-cluster distances for seven clusters in mungbean.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	63.29 (7.96)	218.80 (14.79)	588.47 (24.26)	140.32 (11.85)	566.87 (23.81)	574.41 (23.97)	574.59 (23.97)
Cluster II		110.29 (10.50)	284.46 (16.87)	230.31 (15.18)	196.66 (14.02)	342.99 (18.52)	345.44 (18.59)
Cluster III			165.25 (12.86)	511.36 (22.61)	285.08 (16.88)	298.37 (17.27)	481.75 (21.95)
Cluster IV				187.85 (13.71)	510.32 (22.59)	597.92 (24.45)	663.76 (25.76)
Cluster V					0.00 (0.00)	401.97 (20.05)	310.79 (17.63)
Cluster VI						0.00 (0.00	158.25 (12.58)
Cluster VII							0.00 (0.00)

to the analysis of variance. Estimates of genetic divergence was done by following Mahalanobis D^2 (1936) analysis and based on the D^2 values the thirty one genotypes were grouped into different clusters.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences between mungbean genotypes for all the characters studied and hence considered for estimation of D^2 values. All the thirty one genotypes were grouped into seven clusters (Table 1 and Fig 1). The maximum number of genotypes were included in cluster II (10 genotypes), followed by cluster III (8 genotypes), cluster IV (6 genotypes) and cluster I (4 genotypes). while the clusters V, VI and VII were solitary clusters consisting of one genotype each. The pattern of group constellation indicated significant variability among the genotypes as observed from the clusters. The genotypes of the same origin were distributed into different clusters indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes. Similar findings were also reported by Appalaswamy (1997), Mannivannan *et al*. (1998) and Rahim (2010) in mungbean. This kind of genetic diversity recorded among the genotypes belonging to the same geographic origin might be due to difference in adoption, selection criteria, selection pressure and environmental condition.

Fig.1. Dendrogram of thirty one mungbean genotypes obtained through Tocher's method of classification

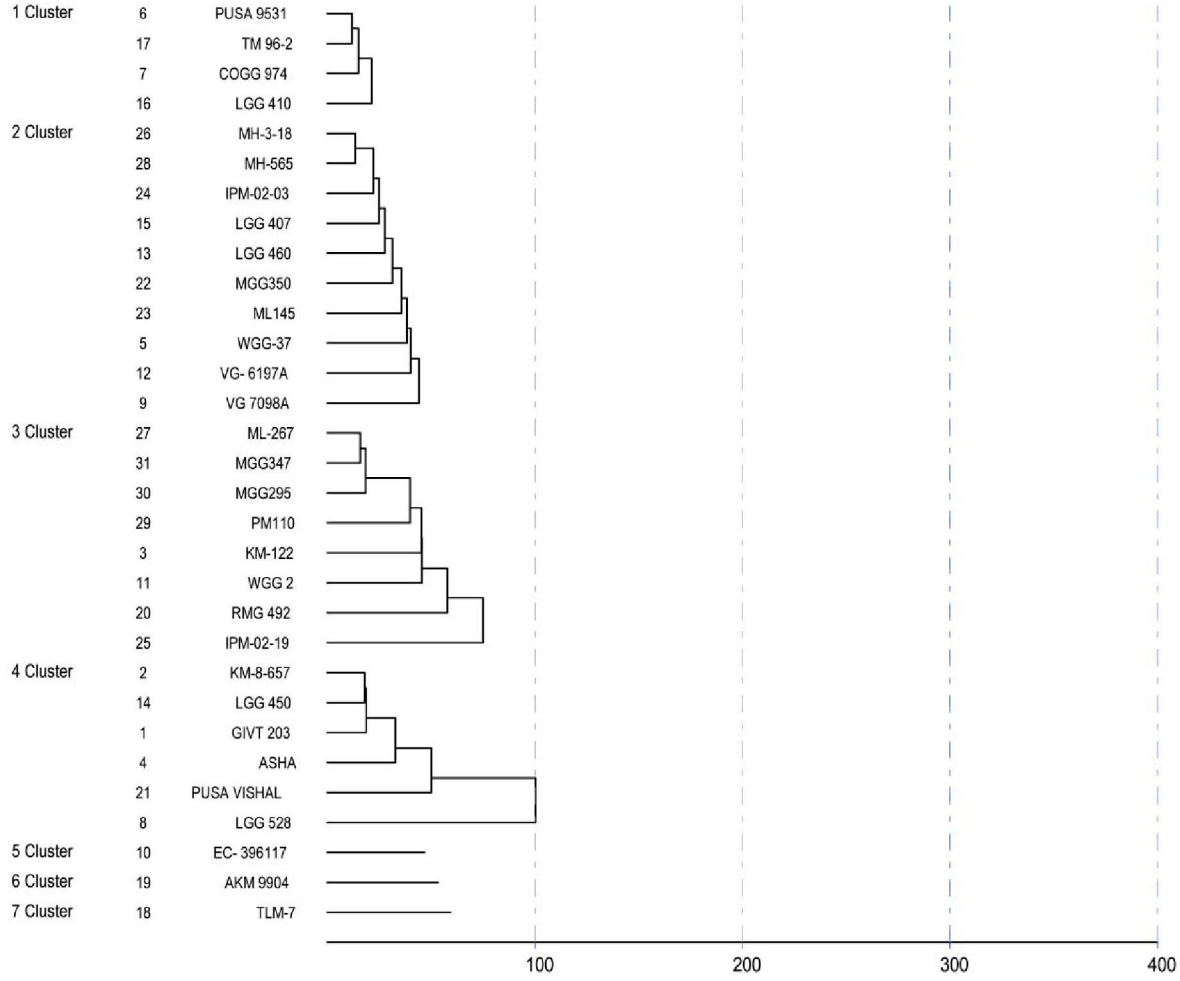

Fig. 2. Intra-cluster (D) and inter-cluster distance (D^2) among seven clusters of mungbean.

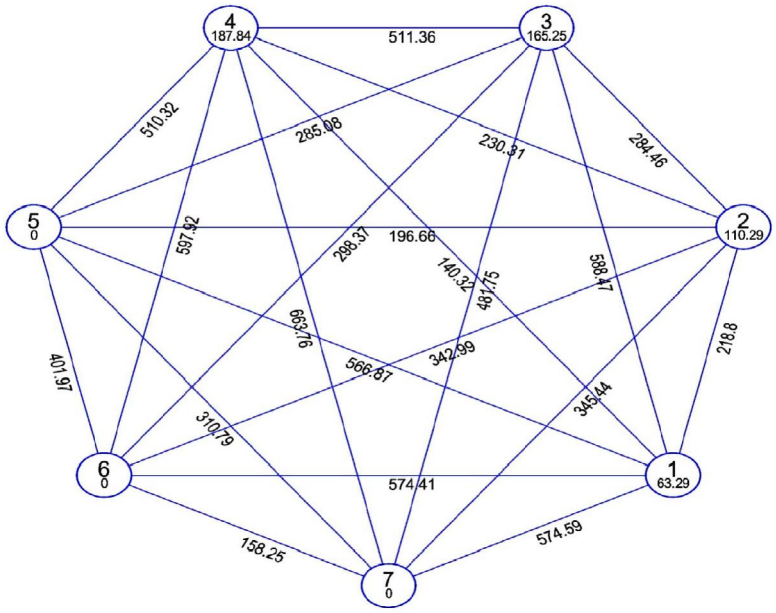

Table 3. Mean performance of the clusters with respect to different characters.

Character / cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters/ plant	No. of Pods/ cluster	No. of pods/ plant	No. of seeds/ pod	100 seed weight (g)	Harvest index (%)	SCMR	Relative water content (%)	Relative injury(%)	Chlorophyll stability index	Specific leaf area (cm^2 g^{-1})	Seed yield/ plant (g)
Cluster I	38.50	63.50	41.04	9.50	3.58	23.17	9.83	3.57	43.03	46.18	83.17	48.21	60.75	112.35	4.70
Cluster II	33.93	62.20	35.31	9.70	3.60	23.20	9.50	4.07	59.33	47.57	85.52	37.13	58.43	117.05	6.49
Cluster III	35.96	65.13	41.84	10.17	3.13	24.75	10.75	4.21	64.90	47.20	83.92	44.50	59.22	132.98	10.64
Cluster IV	37.67	63.83	44.13	9.11	4.94	22.17	10.17	3.66	47.83	44.24	83.67	34.95	58.49	126.85	5.24
Cluster V	32.67	60.00	34.67	9.33	3.00	20.67	8.33	5.65	79.48	49.47	84.62	27.86	51.55	120.26	6.72
Cluster VI	35.00	64.33	35.77	10.33	2.67	26.00	10.33	3.74	64.28	40.43	86.76	71.47	93.77	99.15	8.35
Cluster VII	29.67	64.33	31.40	10.00	2.67	14.67	10.00	5.13	66.81	46.33	82.32	84.81	79.34	106.23	6.10

The inter cluster distance ranged from 140.32 (cluster I and IV) to 663.76 (cluster IV and VII) (Table 2 and Fig 2). Maximum distance was observed between the cluster IV and VII and was closely followed by IV and VI (597.92) and cluster I and VII (574.59). Based on the diversity values it could be predicted that hybridization between the genotypes of cluster IV and VII, cluster I and IV might result in useful transgressive seggregants and high level of heterotic expression for seed yield, drought stress and its components.

Cluster III recorded the highest mean for days to maturity, number of seeds per pod and seed yield per plant (Table 3). Cluster V recorded highest mean value for 100 seed weight, harvest index, SCMR and relative injury, while cluster VI recorded highest mean values for number of clusters per plant, number of pods per plant, relative water content, chlorophyll stability index and specific leaf area.

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Loganathan *et al*., 2001) and the contribution towards genetic divergence is represented in table 4. It was observed that among all the traits, contribution of seed yield per plant was maximum (40.43%) followed by harvest index (21.72%) and relative injury (16.34%). In addition, chlorophyll stability index (CSI) (7.31%) and specific leaf area (6.67%) also contributed towards total divergence. Similar results were also reported by Appalaswamy and Reddy (2004) for seed yield in mungbean.

It is well known that crosses between divergent parents usually produce greater heterotic effect and transgressive seggregants in further generations than closely related ones. Considering the D^2 values and the importance of characters towards total divergence, the present study indicated that hybridization programme may be initiated between PUSA VISHAL X TLM 7 (cluster IV X cluster VII) in order to get transgressive seggregants for drought tolerance since, these genotypes showed maximum diversity among themselves with desirable yield and drought parameters. Similarly, the crosses between genotypes ASHA X TLM 7 (cluster IV X cluster VII), IPM-02-19 X COGG 974 (cluster III X cluster I) and TLM 7 X COGG 974 (cluster VII X cluster I) could also be suggested for the exploitation of transgressive seggregants for high yield coupled with drought tolerance. Therefore, it was concluded that more emphasis should be given on cluster III for selecting genotypes as parents for crossing with genotypes of other clusters which may produce new recombinants with desired traits.

Table 4. Contribution of different quantitative characters to diversity in mungbean.

S.No	Character	Times ranked first	Contribution (%)
1.	Days to 50% flowering	4	0.86
2.	Plant height (cm)	4	0.86
3.	Days to maturity	3	0.65
4.	No. of clusters/ plant	0	0.00
5.	No. of pods/ cluster	0	0.00
6.	No. of pods/ plant	6	1.29
7.	No. of seeds/ pod	0	0.00
8.	100 seed weight (g)	13	2.80
9.	Harvest index (%)	101	21.72
10.	SPAD	5	1.08
11.	Relative Water Content (%)	0	0.00
12.	Relative Injury (%)	76	16.34
13.	CSI	34	7.31
14.	Specific leaf area (cm^2 g^{-1})	31	6.67
15.	Seed Yield (g)	188	40.43

LITERATURE CITED

Appalaswamy A 1997 Genetic divergence stability and combining ability studies in mungbean (*Vigna radiata* L. Wilezech) *Ph.D. Thesis*, Acharya N.G. Ranga Agricultural University, Hyderabad.

Appalaswamy A and Reddy G L K 2004 Genetic divergence and heterosis studies in mungbean (*Vigna radiata* (L.) Wilczek).*Legume Research*, 27(2): 115-118.

Loganathan, Saravanan, PK and Ganesan J 2001 Genetic analysis of yield and related components in greengram (*Vigna radiata* L.).*Research on Crops,* 1: 34-36.

Mahalnobis K C 1936 On the generalized distances in statistics. *Proceedings of National Institute of Sciences,* India, 2: 49-55.

Mannivannan N, Murugan E, Viswanathan PL and Dhanakodi C V 1998 *Legume Research,* 21(2): 131- 133.

Rahim M A, Mia AA, Mahmud F, Zeba N and Afrin K S 2010 Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* (L). Wilczek).*Plant Omics Journal,* 3(1): 1-6.

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